Amendments to the Specification

On page 1, before "Background of the Invention": please add the following paragraph:

This application claims priority from U.S. Provisional Application Serial No. 60/268,370, filed 02/14/2001.

Please replace the paragraph bridging pages 15 and 16 with the following amended paragraph:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol. 48*:444-453 (1970) algorithm which has been incorporated into the GAP program in the GCG software package (available on the Worldwide web at the URL ~~http://www.~~gcg.com), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at http://www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases, for example, to identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul *et al.* (1990) *J. Mol. Biol. 215*:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to human or murine HPRG nucleic acid molecules. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to HPRG protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res. 25*:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*,, XBLAST and NBLAST) can be used. See Worldwide web URL ~~http://www.~~ncbi.nlm.nih.gov.

Please amended the paragraph beginning at page 27, line 27, and ending at page 28, line 14, as follows:

A preferred type of chemical derivative of the peptides described herein is a peptidomimetic compound which mimics the biological effects of HPRG or of a biologically active peptide thereof. A peptidomimetic agent may be an unnatural peptide or a non-peptide agent that recreates the stereospatial properties of the binding elements of HPRG such that it has the binding activity or biological activity of HPRG. Similar to biologically active HPRG peptides, a peptidomimetic will have a binding face (which interacts with any ligand to which HPRG binds) and a non-binding face. Again, similar to HPRG or its peptide, the non-binding face of a peptidomimetic will contain functional groups which can be modified by various therapeutic and diagnostic moieties without modifying the binding face of the peptidomimetic ~~(again, I do not see the description of this for the protein and peptide) ???~~. A preferred embodiment of a peptidomimetic would contain an aniline on the non-binding face of the molecule. The NH_2-group of an aniline has a pKa ~ 4.5 and could therefore be modified by any NH_2 - selective reagent without modifying any NH_2 functional groups on the binding face of the peptidomimetic. Other peptidomimetics may not have any NH_2 functional groups on their binding face and therefore, any NH_2 , without regard for pK_a could be displayed on the non-binding face as a site for conjugation. In addition other modifiable functional groups, such as -SH and -COOH could be incorporated into the non-binding face of a peptidomimetic as a site of conjugation. A therapeutic or diagnostic moiety could also be directly incorporated during the synthesis of a peptidomimetic and preferentially be displayed on the non-binding face of the molecule.